I. AMENDMENT

Amendment to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application:

Claims 1 – 31 (canceled)

32. (PREVIOUSLY PRESENTED) An isolated polynucleotide fragment comprising a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity, wherein said polypeptide shares at least 95% homology with SEQ ID NO:44 as determined using default parameters of a DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin.

33. (PREVIOUSLY PRESENTED) The polynucleotide fragment of claim 32, wherein said polynucleotide comprises the coding region, nucleotides 594 to 2198, of SEQ ID NO:43.

34. (PREVIOUSLY PRESENTED) The polynucleotide fragment of claim 32, wherein said polynucleotide is as set forth in SEQ ID NO:43.

35. (PREVIOUSLY PRESENTED) The polynucleotide fragment of claim 32, wherein said polynucleotide sequence includes a segment of SEQ ID NO:43, said segment encodes said polypeptide having said heparanase catalytic activity.

36. (PREVIOUSLY PRESENTED) The polynucleotide fragment of claim 32, wherein said polypeptide includes an amino acid sequence as set forth in SEQ ID NO:44.

37. (PREVIOUSLY PRESENTED) The polynucleotide fragment of claim 32, wherein said polypeptide includes a segment of SEQ ID NO:44 said segment harbors said heparanase catalytic activity.

38. (PREVIOUSLY PRESENTED) The polynucleotide fragment of claim 32, wherein said polynucleotide sequence is selected from the group consisting of double stranded DNA, single stranded DNA and RNA.

39. (PREVIOUSLY PRESENTED) An isolated polynucleotide sequence as set forth in SEQ ID NO:43.

40. (CURRENTLY AMENDED) An isolated polynucleotide sequence at least 95% homologous to ~~the coding region~~[[,]] nucleotides 594 to 2198[[,]] of SEQ ID NO:43[[,]] ~~as shown in SEQ ID NO:45~~, as determined using default parameters of a DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin, wherein said polynucleotide sequence encodes a polypeptide having heparanase catalytic activity.

41. (PREVIOUSLY PRESENTED) A vector comprising an isolated polynucleotide sequence encoding a polypeptide having heparanase catalytic activity, wherein said polypeptide shares 95% homology with SEQ ID NO:44 as determined using default parameters of a DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin.

42. (PREVIOUSLY PRESENTED) The vector of claim 41, wherein said polynucleotide comprises the coding region, nucleotides 594 to 2198, of SEQ ID NO:43.

43. (PREVIOUSLY PRESENTED) The vector of claim 41, wherein said polynucleotide sequence is as set forth in SEQ ID NO:43.

44. (PREVIOUSLY PRESENTED) The vector of claim 41, wherein said polynucleotide sequence includes a segment of SEQ ID NO:43, said segment encodes said polypeptide having said heparanase catalytic activity.

45. (PREVIOUSLY PRESENTED) The vector of claim 41, wherein said polypeptide includes an amino acid sequence as set forth in SEQ ID NO:44.

46. (PREVIOUSLY PRESENTED) The vector of claim 41, wherein said polypeptide includes a segment of SEQ ID NO:44 said segment harbors said heparanase catalytic activity.

47. (PREVIOUSLY PRESENTED) The vector of claim 41, wherein said polynucleotide sequence is selected from the group consisting of double stranded DNA, single stranded DNA and RNA.

48. (PREVIOUSLY PRESENTED) The vector of claim 41, wherein said vector is a baculovirus vector.

49. (PREVIOUSLY PRESENTED) A host cell comprising an exogenous polynucleotide fragment including an isolated polynucleotide sequence encoding a polypeptide having heparanase catalytic activity, wherein said polypeptide shares 95% homology with SEQ ID NO:44, as determined using default parameters of a DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin.

50. (PREVIOUSLY PRESENTED) The host cell of claim 49, wherein said polynucleotide comprises nucleotides 594 to 2198, of SEQ ID NO:43.

51. (PREVIOUSLY PRESENTED) The host cell of claim 49, wherein said polynucleotide sequence is as set forth in SEQ ID NO:43.

52. (PREVIOUSLY PRESENTED) The host cell of claim 49, wherein said polynucleotide sequence includes a segment of SEQ ID NO:43, said segment encodes said polypeptide having said heparanase catalytic activity.

53. (PREVIOUSLY PRESENTED) The host cell of claim 49, wherein said polypeptide includes an amino acid sequence as set forth in SEQ ID NO:44.

54. (PREVIOUSLY PRESENTED) The host cell of claim 49, wherein said polypeptide includes a segment of SEQ ID NO:44 said segment harbors said heparanase catalytic activity.

55. (PREVIOUSLY PRESENTED) The host cell of claim 49, wherein said polynucleotide sequence is selected from the group consisting of double stranded DNA, single stranded DNA and RNA.

56. (CURRENTLY AMENDED) A host cell comprising the polynucleotide fragment of claim 32 ~~expressing a purified recombinant heparanase, wherein said recombinant heparanase shares 95% homology with SEQ ID NO:44 as determined using default parameter of a DNA sequence analysis software package developed by the Genetic Computer (Group (GCG) at the University of Wisconsin~~.

57. (PREVIOUSLY PRESENTED) A heparanase overexpression system comprising a cell overexpressing heparanase catalytic activity, wherein said heparanase catalytic activity is effected by a purified recombinant heparanase sharing at least 95% homology with SEQ ID NO:44 as determined using default parameters of a DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin.

58. (PREVIOUSLY PRESENTED) The host cell of claim 49, wherein said cell is an insect cell.

59. (PREVIOUSLY PRESENTED) An isolated polynucleotide fragment comprising a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity, wherein said polypeptide shares at least 95% homology with SEQ ID NO:44 as determined using default parameters of a DNA sequence analysis software package

developed by the Genetic Computer Group (GCG) at the University of Wisconsin, wherein said polypeptide is characterized by being about 50 or about 65 kDa, and said polypeptide is characterized by being capable of being purified with a purification procedure initiated with Heparin-Sepharose chromatography, followed by gel filtration and pooling of active column fractions, wherein a quantity of said polypeptide after said purification correlates with heparanase activity in said pooled active column fractions.